

REMARKS

Applicant respectfully requests an interview in accordance with 37 C.F.R. § 1.133(a)(1) prior to the next office communication. The Examiner is invited to contact the undersigned in an effort to arrange a mutually agreeable time therefor.

The instant reply is filed in response to the office action dated December 4, 2002 in the above-identified application.

The change in the specification corrects a clerical error. Support for this change is found in the specification as filed at page 38, lines 2-4.

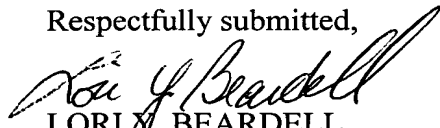
In the Office Action the Claims were subject to a lack of unity of invention rejection and divided into 94 independent groups. Applicants elect the Claims of Group I (Claims 1, 3-19, 26, 28-33, 44, and 45), without traverse, and the invention of Group u (SEQ ID NO:66), with traverse.

Appendix A and B, filed herewith, provide additional evidence regarding the relationship between the claimed amino acid sequences. The subject office action includes 20 nucleotide sequences and the 20 amino acid sequences encoded by them (Groups a-t), and a consensus sequence generated from aligning the 20 amino acid sequences (Group u). The consensus sequence is shown in the subject application as SEQ ID NO:66. The 65 positions at which there is at least one difference among the 20 amino acid sequences is indicated as Xaa in SEQ ID NO: 66. Each of the Xaa positions is defined in the specification as filed at page 41, line 16 through page 42, line 11.

In the accompanying Appendix A, the amino acids which differ among the 20 isoflavone synthase amino acid sequences are boxed in black and written in white. This alignment shows that out of 521 amino acids, there are only 65 differences among the different isoflavone synthases. Furthermore as indicated in Table 2 at pages 40 and 41 of the application as filed, and in the accompanying Appendix B, the 20 amino acid sequences are between 95.6 and 99.0% identical to each other. Thus, the amino acid sequences of Groups a-u have the same function (as indicated by the assays shown in Examples 5, 6, and 7 of the application as filed), and are more than 95% identical to each other. Thus, there is unity of invention among Groups a-u.

In view of the foregoing amendments and remarks, early and favorable notification of allowance of claims 1, 3-19, 26, 28-33, 44, and 45 is earnestly solicited.

Respectfully submitted,


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Dated: April 1, 2003

VERSION WITH MARKING TO SHOW CHANGES MADE

In showing the changes, deleted material is shown in brackets, and inserted material is shown underlined.

IN THE SPECIFICATION:

Please replace the paragraph beginning at page 11, line 11:

SEQ ID NO:30 is the deduced amino acid sequence of an entire mung bean isoflavone synthase derived from SEQ ID NO:[30]29.

APPENDIX A



Clustal V alignment of the amino acid sequences corresponding to isoflavone synthases from soybean (SEQ ID NO:2 and SEQ ID NO:10), alfalfa (SEQ ID NO:16, SEQ ID NO:57, and SEQ ID NO:59), hairy vetch (SEQ ID NO:18), lentil (SEQ ID NO:20 and SEQ ID NO:22), mung bean (SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, and SEQ ID NO:30), red clover (SEQ ID NO:32 and SEQ ID NO:34), snow pea (SEQ ID NO:36), white clover (SEQ ID NO:38 and SEQ ID NO:40), sugar beet (SEQ ID NO:48 and SEQ ID NO:61), lupine (SEQ ID NO:55), and the consensus sequence (SEQ ID NO:66). Amino acids that are different in at least one sequence are boxed in black and written in white. The program uses dashes to maximize the alignment.

1	SEQ ID NO:2	M L L E L A L G L	F	V L A L F	L	H L R P T P	S	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L	
	SEQ ID NO:10	M L L E L A L G L	L	V L A L F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L	
	SEQ ID NO:16	-----	-	-----	F	L	H L R P T P	S	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L
	SEQ ID NO:18	-----	-	-----	F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L
	SEQ ID NO:20	-----	-	-----	F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	P	H L L K D K L L H Y A	L
	SEQ ID NO:22	-----	-	-----	F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L
	SEQ ID NO:24	M L L E L A L G L	L	V L A L F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L	
	SEQ ID NO:26	M L L E L A L G L	L	V L A L F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L	
	SEQ ID NO:28	M L L E L A L G L	L	V L A L F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L	
	SEQ ID NO:30	M L L E L A L G L	L	V L A L F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L	
	SEQ ID NO:32	M L L E L A L G L	L	V L A L F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L	
	SEQ ID NO:34	M L L E L A L G L	L	V L A L F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L	
	SEQ ID NO:36	M L L E L A L G L	F	V L A L F	L	H L R P T P	S	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L	
	SEQ ID NO:38	-----	-	-----	S	L	H L R P T P	S	A	I	S K A L R H L P N P P S P	R	P R L P F I G H	L	H L L K D K L L H Y A	P
	SEQ ID NO:40	-----	-	-----	F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L
	SEQ ID NO:61	-----	-	-----	F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L
	SEQ ID NO:55	-----	-	-----	F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L
	SEQ ID NO:57	-----	-	-----	F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L
	SEQ ID NO:59	-----	-	-----	F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L
	SEQ ID NO:48	-----	-	-----	F	L	H L R P T P	T	A	K	S K A L R H L P N P P S P	K	P R L P F I G H	L	H L L K D K L L H Y A	L
	SEQ ID NO:66	M L L E L A L G L	X	V L A L F	X	H L R P T P	X	A	X	S K A L R H L P N P P S P	X	P R L P F I G H	X	H L L K D K L L H Y A	X	

APPENDIX A (Continued)



61	SEQ	ID NO: 2	IDLSKKHGPLFS	LS	FGSMPTVVASTPELFLFLQ	TH	EATSF	N	TRFQ TSA	I	R	R	LTYD	NS	VA
	SEQ	ID NO: 10	IDLSKKHGPLFS	LY	FGSMPTVVASTPELFLFLQ	TH	EATSF	N	TRFQ TSA	I	R	R	LTYD	SS	VA
	SEQ	ID NO: 16	IDLSKKHGPLFS	IS	FGSMPTVVASTPELFLFLQ	TH	EATSF	N	TRFQ TSA	T	R	R	LTYD	NS	VA
	SEQ	ID NO: 18	IDLSKKHGPLFS	LY	FGSMPTVVASTPELFLFLQ	TH	EATSF	N	TRFQ TSA	I	R	R	LTYD	SL	VA
	SEQ	ID NO: 20	IDLSKKHGPLFS	LY	FGSMPTVVASTPELFLFLQ	TH	EATSF	N	TRFQ TSA	I	R	R	LTYD	SS	VA
	SEQ	ID NO: 22	IDLSKKHGPLFS	LY	FGSMPTVVASTPELFLFLQ	TH	EATSF	N	TRFQ TSA	I	R	R	LTYD	SS	VA
	SEQ	ID NO: 24	IDLSKKHGPLFS	LY	FGSMPTVVASTPELFLFLQ	TH	EATSF	N	TRFQ TSA	I	R	R	LTYD	SS	VA
	SEQ	ID NO: 26	IDLSKKHGPLFS	LY	FGSMPTVVASTPELFLFLQ	TH	EATSF	N	TRFQ TSA	I	R	R	LTYD	SS	VA
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	SEQ	ID NO: 36	IDLSKKHGPLFS	LS	FGSMPTVVASTPELFLFLQ	AH	EATSF	S	TRFQ TSA	V	R	R	LTYD	NS	VA
	SEQ	ID NO: 38	IDLSKKHGPLFS	LS	FGSMPTVVASTPELFLFLQ	TH	EATSF	N	TRFQ TSA	I	R	H	LTYD	NS	VA
	SEQ	ID NO: 40	IDLSKKHGPLFS	LY	FGSMPTVVASTPELFLFLQ	TH	EATSF	N	TRFQ TSA	I	R	R	LTYD	NS	VA
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	SEQ	ID NO: 66	IDLSKKHGPLFS	XX	FGSMPTVVASTPELFLFLQ	XX	EATSF	X	TRFQ TSA	X	R	X	LTYD	XX	VA

APPENDIX A (Continued)



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SEQ ID NO: 18		MV	P	F	GPYW	K	FVRKLIMNDLLNATTN	K	LRPLRTQQIRK	F	LR	V	MAQ	G	AEA	Q	KPLD	L	TEELL
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SEQ ID NO: 38		MV	P	F	GPYW	K	FVRKLIMNDLLNATTN	K	LRPLRTQQIRK	F	LR	V	MAQ	S	AEA	Q	KPLD	V	TEELL
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SEQ ID NO: 55		RV	P	F	GPYW	K	FVRKLIMNDLLNATTN	K	LRPLRTQQIRK	F	LR	V	MAQ	G	AEA	Q	KPLD	L	TEELL
SEQ ID NO: 57		MA	P	F	GPYW	K	FVRKLIMNDLLNATTN	K	LRPLRTQQIRK	F	LR	V	MAQ	G	AEA	Q	KPLD	L	TEELL
SEQ ID NO: 59		MV	P	F	GPYW	K	FVRKLIMNDLLNATTN	K	LRPLRTQQIRK	L	LR	V	MAQ	G	AEA	Q	KPLD	L	TEELL
SEQ ID NO: 48		MV	P	F	GPYW	K	FVRKLIMNDLLNATTN	K	LRPLRTQQIRK	F	LR	A	MAQ	G	AEA	R	KPLD	L	TEELL
SEQ ID NO: 66		XX	P	X	GPYW	X	FVRKLIMNDLLNATTN	X	LRPLRTQQIRK	X	LR	X	MAQ	X	AEA	X	KPLD	X	TEELL



APPENDIX A (Continued)

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APPENDIX A (Continued)



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SEQ	ID	NO:	18	DPVVERVIKKRR	E	IVRRR	K	NGE	VV	EGE	V	SGV	F	LDTLLEFAEDET	T	EIKITKD	HI	KGLVVD
SEQ	ID	NO:	20	DPVVERVIKKRR	E	IVRRR	K	NGE	VV	EGE	A	SGV	F	LDTLLEFAEDET	M	EIKITKE	QI	KGLVVD
SEQ	ID	NO:	22	DPVVERVIKKRR	E	IVRRR	K	NGE	VV	EGE	V	SGV	F	LDTLLEFAEDET	M	EIKITKD	HI	KGLVVD
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SEQ	ID	NO:	66	DPVVERVIKKRR	X	IVRRR	X	NGE	XX	EGE	X	SGV	X	LDTLLEFAEDET	X	EIKITKD	XX	KGLVVD

APPENDIX A (Continued)



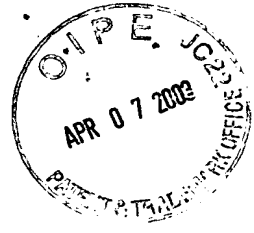
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SEQ	ID	NO:	26	F	FSAG	T	DSTA	VA	TEWALAEELINNP	K	VL	E	KAREE	V	YSVVGKD	R	LVDEVD	TQNL	PYIRAI	VK	
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SEQ	ID	NO:	48	F	FSAG	T	DSTA	VA	TEWALAEELINNP	K	VL	E	KAREE	V	YSVVGKD	R	LVDEVD	TQNL	PYIRAI	VK	
SEQ	ID	NO:	66	X	FSAG	X	DSTA	XX	TEWALAEELINNP	X	VL	X	KAREE	X	YSVVGKD	X	LVDEVD	TQNL	PYIRAI	VK	

APPENDIX A (Continued)



361	SEQ	ID	NO:	2	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	VL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	420
	SEQ	ID	NO:	10	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	IL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	16	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	VL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	18	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	IL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	20	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	H	V	I	PEGAL	VL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	22	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	C	V	T	PEGAL	IL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	24	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	IL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	26	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	IL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	28	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	IL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	30	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	IL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	32	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	IL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	34	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	IL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	36	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	VL	ENVWQVG	K	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	38	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	VL	ENVWQVG	R	D	P	KYWDRPSE	S	RPERFLE	
	SEQ	ID	NO:	40	ETFRMHPPPLPVVKKKC	T	EEC	G	ING	Y	V	I	PEGAL	VL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	61	ETFRMHPPPLPVVKKKC	I	EEC	E	ING	Y	V	I	PEGAL	IL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	55	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	IL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	57	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	IL	ENVWQVG	R	D	S	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	59	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	IL	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	48	ETFRMHPPPLPVVKKKC	T	EEC	E	ING	Y	V	I	PEGAL	IP	ENVWQVG	R	D	P	KYWDRPSE	F	RPERFLE	
	SEQ	ID	NO:	66	ETFRMHPPPLPVVKKKC	X	EEC	X	ING	X	V	X	PEGAL	XX	ENVWQVG	X	D	X	KYWDRPSE	X	RPERFLE	

APPENDIX A (Continued)



421	SEQ	ID	NO:	2	T	G	AEGEA	GP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	480
	SEQ	ID	NO:	10	T	G	AEGEA	GP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	16	T	G	AEGEA	GP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	18	T	G	AEGEA	RP	LDLRG	Q	HFQLLPFGSGR	G	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	20	T	G	AEGEA	GP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	22	T	G	AEGEA	RP	LDLRG	R	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	24	T	G	AEGEA	RP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	26	T	G	AEGEA	RP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	28	T	G	AEGEA	RP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	30	T	G	AEGEA	RP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	32	T	G	AEGEA	RP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	34	T	G	AEGEA	RP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	36	T	G	AEGEA	GP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	38	T	G	AEGEA	GP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	S	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	40	T	G	AEGEA	GP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	61	T	G	AEGEA	RL	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	55	T	E	AEGEA	RP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	I	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	57	T	G	AEGEA	RP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	59	T	G	AEGEA	RP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	M	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	48	T	G	AEGEA	RP	LDLRG	Q	HFQLLPFGSGR	R	MCPGV	N	LATSG	T	ATLLASLIQCFDLQVLGPQG	
	SEQ	ID	NO:	66	T	X	AEGEA	XX	LDLRG	X	HFQLLPFGSGR	X	MCPGV	X	LATSG	X	ATLLASLIQCFDLQVLGPQG	

APPENDIX A (Continued)



481 522

SEQ ID NO: 2	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS-
SEQ ID NO: 10	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS-
SEQ ID NO: 16	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARI-----
SEQ ID NO: 18	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARI-----
SEQ ID NO: 20	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARI-----
SEQ ID NO: 22	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARI-----
SEQ ID NO: 24	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLSK
SEQ ID NO: 26	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS-
SEQ ID NO: 28	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS-
SEQ ID NO: 30	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS-
SEQ ID NO: 32	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS-
SEQ ID NO: 34	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS-
SEQ ID NO: 36	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS-
SEQ ID NO: 38	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARI-----
SEQ ID NO: 40	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARI-----
SEQ ID NO: 61	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARI-----
SEQ ID NO: 55	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARI-----
SEQ ID NO: 57	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARI-----
SEQ ID NO: 59	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARI-----
SEQ ID NO: 48	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARI-----
SEQ ID NO: 66	ILKGGDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS-

APPENDIX B

Pair Distances of protein.MEG ClustalV (PAM250)

Percent Similarity in upper triangle
Percent Divergence in lower triangle

SEQ ID	2	10	16	18	20	22	24	26	28	30	32	34	36	38	40	61	55	57	59	48	
2	***	96.7	99.0	96.2	98.8	96.4	96.7	96.7	96.7	96.7	96.4	96.7	99.0	98.4	99.0	96.6	96.2	96.2	96.6	95.6	2
10		3.3	***	95.8	98.2	96.8	98.4	99.0	99.0	99.0	98.7	99.0	95.8	95.2	97.0	98.6	98.2	98.2	98.6	97.6	10
16		1.0	4.3	***	95.2	97.8	95.4	96.0	96.0	96.0	95.6	96.0	98.2	97.4	98.0	95.6	95.2	95.2	95.6	94.6	16
18		3.9	1.8	5.0	***	96.2	98.2	98.8	99.2	98.8	98.8	99.2	95.2	94.6	96.4	98.4	98.0	98.4	98.8	97.4	18
20		1.2	3.3	2.2	3.9	***	96.6	97.0	97.0	97.0	96.6	97.0	97.8	97.2	98.6	96.6	96.2	96.2	96.6	95.6	20
22		3.7	1.6	4.8	1.8	3.5	***	99.0	99.0	99.0	98.6	99.0	95.4	94.8	96.6	98.6	98.2	98.2	98.6	97.6	22
24		3.1	1.0	4.1	1.2	3.1	1.0	***	99.4	99.4	99.0	99.4	96.0	95.4	97.6	99.2	98.8	98.8	99.2	98.2	24
26		3.1	1.0	4.1	1.2	3.1	1.0	0.4	***	99.4	99.0	99.4	96.0	95.4	97.2	99.2	98.8	98.8	99.2	98.6	26
28		3.1	1.0	4.1	0.8	3.1	1.0	0.4	***	99.4	99.4	99.8	96.0	95.4	97.2	99.2	98.8	99.2	99.6	98.2	28
30		3.1	1.0	4.1	1.2	3.1	1.0	0.4	0.4	***	99.0	99.4	96.0	95.4	97.2	99.2	98.8	98.8	99.2	98.2	30
32		3.5	1.4	4.5	1.2	3.5	1.4	0.8	0.4	0.8	***	99.4	95.6	95.0	96.8	98.8	98.4	98.8	99.4	97.8	32
34		3.1	1.0	4.1	0.8	3.1	1.0	0.4	0.0	0.4	0.4	***	96.0	95.4	97.2	99.2	98.8	99.2	99.6	98.2	34
36		1.0	4.4	1.8	5.0	2.2	4.8	4.4	4.2	4.2	4.6	4.2	***	97.4	98.0	95.6	95.2	95.2	95.6	94.6	36
38		1.6	5.0	2.5	5.4	2.7	5.2	4.8	4.8	4.8	5.2	4.8	2.7	***	97.4	95.0	94.8	94.6	95.0	94.0	38
40		1.0	3.1	2.0	3.7	1.4	3.5	2.4	2.9	2.9	3.3	2.9	2.0	2.5	***	96.8	96.4	96.4	96.8	95.8	40
61		3.5	1.4	4.5	1.6	3.5	1.4	0.8	0.8	0.8	1.2	0.8	4.5	5.0	3.3	***	98.4	98.4	98.8	97.8	61
55		3.9	1.8	5.0	2.0	3.9	1.8	1.2	1.2	1.2	1.6	1.2	5.0	5.2	3.7	1.6	***	98.0	98.4	97.4	55
57		3.9	1.8	5.0	1.6	3.9	1.8	1.2	0.8	1.2	1.2	0.8	5.0	5.4	3.7	1.6	2.0	***	98.8	97.4	57
59		3.5	1.4	4.6	1.2	3.5	1.4	1.0	0.4	0.8	0.6	0.4	4.8	5.0	3.3	1.2	1.6	1.2	***	97.8	59
48		4.6	2.5	5.6	2.7	4.6	2.5	1.8	1.4	1.8	2.2	1.8	5.6	6.1	4.3	2.2	2.7	2.7	2.2	***	48
	2	10	16	18	20	22	24	26	28	30	32	34	36	38	40	61	55	57	59	48	